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=> s gill?/au
L4      118104 GILL?/AU

=> s l4 and forensic#
L5         397 L4 AND FORENSIC#

=> s l5 and l1
L6           7 L5 AND L1

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7           5 DUP REM L6 (2 DUPLICATES REMOVED)

=> d 1-5 bib ab

L7   ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2002 ACS
AN   2001:781166  CAPLUS
DN   135:328103
TI   Improvements in and relating to analysis of DNA samples
IN   Gill, Peter
PA   Secretary of State for the Home Department, UK
SO   PCT Int. Appl., 68 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
     ---------------    ----  --------      ---------------  --------
PI   WO 2001079541      A2    20011025      WO 2001-GB1657   20010412
     WO 2001079541      A3    20020530
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
             HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
             LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
             RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
             VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002007248 A1 20020117 US 2001-834822 20010413

PRAI GB 2000-9294 A 20000415

AB The invention provides an improved method for obtaining information about DNA anal. of samples of uncertain origin by establishing the likelihood that they arose in certain manners compared with other possible manners. In this way all of the anal. information is taken into account and likelihood ratios are provided to express the results. The invention is particularly useful in analyzing small DNA samples or DNA samples where the contribution from one or more sources is small. Math. models for the anal. of allele frequencies in **forensic** samples are presented.

L7 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2002 ACS

AN 2001:472973 CAPLUS

DN 135:72116

TI A method for indicating the likelihood that a DNA mixture arose from sources of a defined type for improvements in **forensic** analysis using **SNP** detection

IN **Gill, Peter**; Hussain, Javaid; Long, Adam; Tully, Gillian

PA Secretary of State for the Home Department, UK

SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001046466	A2	20010628	WO 2000-GB4922	20001221
WO 2001046466	A3	20020228		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002009725 A1 20020124 US 2000-745687 20001222

PRAI GB 1999-30307 A 19991222

AB The invention concerns improvements in and relating to identification, particularly in the field of **forensic** science, and particular relating to identification techniques that shows greater sensitivity and specificity based on the use of **single nucleotide polymorphisms** (**SNP**). The invention provides a method for obtaining addnl. information about DNA mixts. arising from a variety of sources and/or a variety of concns. In particular, the invention provides a method for indicating the likelihood that a DNA mixt. arose from sources of a defined type where: the DNA mixt. is formed by DNA samples from more than one source. The method involves the detn. of the identity of the alleles present at a locus for the DNA in the mixt.; detg. a first probability function for the situation where the DNA mixt. is formed from samples arising from the given person and from a first other person; detg. a second probability function for the situation where the DNA mixt. is formed from samples arising from a second other person and a first other person; using the first probability function as numerator and the second probability function as denominator in detg. a likelihood ratio for the mixt. having arisen from the defined type of sources considered in the first probability function; detg. such likelihood ratios for a plurality of loci; and combining the likelihood ratios to give a combined

likelihood ratio for the mixt. having arisen from the defined type of sources considered in the first probability function.

L7 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2002 ACS
AN 2001:78556 CAPLUS
DN 134:142716
TI Increased sensitivity and specificity in detection of **single nucleotide polymorphisms** by PCR
IN **Gill, Peter**; Hussain, Javaid; Long, Adam
PA The Secretary of State for the Home Department, UK
SO PCT Int. Appl., 92 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001007640	A2	20010201	WO 2000-GB2795	20000724
	WO 2001007640	A3	20011018		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1196623	A2	20020417	EP 2000-948138	20000724
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, MC, IE, SI, LT, LV, FI, RO				
PRAI	GB 1999-17307	A	19990723		
	GB 2000-9187	A	20000414		
	WO 2000-GB2795	W	20000724		

AB A method for detection of known **single nucleotide polymorphisms** in a DNA sample, e.g. in **forensic** identification, that shows greater sensitivity and specificity is described. The method is a form of nested PCR in which target sequences are amplified with one set of primers and these primary amplification products are then amplified with a second set of primers, optionally after the first set of amplification products have been divided into aliquots. The secondary amplification products are then analyzed. The set of primers used in the first round of amplification may have two domains: one is locus specific and the second domain is common to all of the primers used in the first round and is used by the primers for the second round of amplification. The two stage amplification allows the use of low concns. of primers to be used and so avoids problems such as primer dimer formation found when high concns. of primers are used. Primers may be labeled with dyes or mol. beacons. Optimization expts. show that the technique is effective with nanogram quantities of DNA and that it trace quantities (1 in 300) of a contaminating DNA can be detected. Use of second stage primers immobilized on glass slides is also demonstrated. An asym. PCR for the second stage in which the reverse primer is omitted is also described.

L7 ANSWER 4 OF 5 MEDLINE DUPLICATE 1
AN 2001263451 MEDLINE
DN 21254824 PubMed ID: 11355396
TI An assessment of the utility of **single nucleotide polymorphisms** (**SNPs**) for **forensic** purposes.
AU **Gill P**
CS Forensic Science Service, Trident Court, 2960 Solihull Parkway, Birmingham

Business Park, Birmingham B37 7YN, UK.
SO INTERNATIONAL JOURNAL OF LEGAL MEDICINE, (2001) 114 (4-5) 204-10.
Journal code: 9101456. ISSN: 0937-9827.
CY Germany: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200109
ED Entered STN: 20011001
Last Updated on STN: 20011001
Entered Medline: 20010927
AB This paper assesses the use of **single nucleotide polymorphisms** (**SNPs**) for **forensic** analysis. It demonstrates that relatively small arrays of approx. 50 loci are comparable to existing short tandem repeat (STR) multiplexes. A quantitative test, however, is a prerequisite for mixture interpretation. In addition, as the mixture proportion becomes low, it will be necessary to distinguish between the allele and background. Relatively small biallelic arrays are also suitable to distinguish between closely related individuals such as brothers.

L7 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2002 ACS
AN 2000:308653 CAPLUS
DN 134:81446
TI An assessment of the utility of **SNPs**
AU **Gill, Peter**; Hussain, Javaid; Millington, Steven; Long, Adam; Tully, Gillian
CS Forensic Science Service, Birmingham, B56QQ, UK
SO International Congress Series (2000), 1193(Progress in Forensic Genetics 8), 405-407
CODEN: EXMDA4; ISSN: 0531-5131
PB Elsevier Science B.V.
DT Journal
LA English
AB There is increasing interest in use of biallelic marker or **single nucleotide polymorphisms** (**SNPs**) for **forensic** purposes. The anal. of **SNPs** for human identification requires the simultaneous anal. of at least 50 loci. One of the biggest challenges is to reliably construct multiplexes, i.e. single tube reactions which are capable of polymerase chain reaction (PCR) of large no. of loci. Here we describe a method that will facilitate the rapid development of the multiplexes needed. Using this method, we have created an eight locus multiplex which detects polymorphisms at PGM, .alpha.1 antitrypsin, Gc and Y-chromosome M2.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 06:51:08 ON 08 AUG 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 06:59:28 ON 08 AUG 2002
L1 16062 S SNP# OR SINGLE(W)NUCLEOTIDE(W)POLYMORPHISM#
L2 76 S L1 AND FORENSIC#
L3 51 DUP REM L2 (25 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 07:03:01 ON 08 AUG 2002

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, JICST-EPLUS' ENTERED AT 07:04:52 ON 08 AUG 2002
L4 118104 S GILL?/AU

L5 397 S L4 AND FORENSIC#
L6 7 S L5 AND L1
L7 5 DUP REM L6 (2 DUPLICATES REMOVED)

=> s l1 and forensic#
L8 96 L1 AND FORENSIC#

=> s l8 not l2
L9 0 L8 NOT L2

=> dup rem l8
PROCESSING COMPLETED FOR L8
L10 58 DUP REM L8 (38 DUPLICATES REMOVED)

=> d 20-58 ti

L10 ANSWER 20 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Inflammatory bowel disease-related polymorphisms and loci on human chromosomes 5131-33 and 19p13

L10 ANSWER 21 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Nucleic acids containing single nucleotide polymorphisms and methods of their use

L10 ANSWER 22 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof

L10 ANSWER 23 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Silent and missense single nucleotide polymorphisms in genes associated with vascular disease and their diagnostic use

L10 ANSWER 24 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Drug target isogenes: polymorphisms in the immunoglobulin E receptor beta chain gene

L10 ANSWER 25 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Increased sensitivity and specificity in detection of **single nucleotide polymorphisms** by PCR

L10 ANSWER 26 OF 58 MEDLINE DUPLICATE 4
TI High-level multiplex DNA amplification.

L10 ANSWER 27 OF 58 MEDLINE DUPLICATE 5
TI Increasing the **forensic** discrimination of mitochondrial DNA testing through analysis of the entire mitochondrial DNA genome.

L10 ANSWER 28 OF 58 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI A novel dimorphism in the human SRY gene: Usefulness in human migration studies.

L10 ANSWER 29 OF 58 MEDLINE DUPLICATE 6
TI Genotools **SNP** manager: a new software for automated high-throughput MALDI-TOF mass spectrometry **SNP** genotyping.

L10 ANSWER 30 OF 58 MEDLINE DUPLICATE 7
TI An assessment of the utility of **single nucleotide polymorphisms** (**SNPs**) for **forensic** purposes.

L10 ANSWER 31 OF 58 MEDLINE DUPLICATE 8
TI Sample size considerations in genetic polymorphism studies.

L10 ANSWER 32 OF 58 MEDLINE DUPLICATE 9
TI Y-chromosome variation in a Norwegian population sample.

L10 ANSWER 33 OF 58 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 10
TI The use of the LightCycler for the detection of Y chromosome **SNPs**

L10 ANSWER 34 OF 58 MEDLINE DUPLICATE 11
TI Y-chromosomal **SNP** haplotype diversity in **forensic** analysis.

L10 ANSWER 35 OF 58 MEDLINE DUPLICATE 12
TI Examination of Y-STR mutations in sex chromosomal abnormality in **forensic** cases.

L10 ANSWER 36 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI DNA Profiling Technologies: Past, Present and Future

L10 ANSWER 37 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof

L10 ANSWER 38 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Primers and probes for **single nucleotide polymorphisms** in the human genome

L10 ANSWER 39 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI New paths in drug research with **SNP** strips and chips, and Maldi TOF

L10 ANSWER 40 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI An assessment of the utility of **SNPs**

L10 ANSWER 41 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Active microelectronic DNA arrays for diagnostics, pharmacogenomic, and drug-discovery applications.

L10 ANSWER 42 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Plastic microfluidic chips for multiplexed genetic analysis.

L10 ANSWER 43 OF 58 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Human mitochondrial genetics.

L10 ANSWER 44 OF 58 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Quantitative analysis of human DNA sequences by PCR and solid-phase minisequencing.

L10 ANSWER 45 OF 58 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI ABI PRISM 3100: A fully automated and high-performance 16-capillary electrophoresis system for fragment analysis applications.

L10 ANSWER 46 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Mitochondrial DNA genetics: implications for **forensic** casework

L10 ANSWER 47 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Biallelic markers in the human genome

L10 ANSWER 48 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Silent and missense **single nucleotide polymorphisms** in genes associated with vascular disease and their uses

L10 ANSWER 49 OF 58 CAPLUS COPYRIGHT 2002 ACS

TI Primers and probes for detection of polymorphisms in human genes and sequence-tagged sites

L10 ANSWER 50 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Methods and compositions for detection or quantification of nucleic acid species

L10 ANSWER 51 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Methods for polymorphism identification and profiling and uses in epidemiology, diagnosis, **forensics** and genetic mapping

L10 ANSWER 52 OF 58 MEDLINE DUPLICATE 13
TI The utility of short tandem repeat loci beyond human identification: implications for development of new DNA typing systems.

L10 ANSWER 53 OF 58 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 14
TI Informativity assessment for biallelic **single nucleotide polymorphisms.**

L10 ANSWER 54 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI **Single nucleotide polymorphism** determination using primer extension and time-of-flight mass spectrometry

L10 ANSWER 55 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI Forensically important genetic markers

L10 ANSWER 56 OF 58 MEDLINE DUPLICATE 15
TI Characterization of mitochondrial DNA using low-stringency single specific primer amplification analyzed by laser induced fluorescence--capillary electrophoresis.

L10 ANSWER 57 OF 58 MEDLINE DUPLICATE 16
TI Testing the feasibility of DNA typing for human identification by PCR and an oligonucleotide ligation assay.

L10 ANSWER 58 OF 58 CAPLUS COPYRIGHT 2002 ACS
TI A multiplex PCR-ligase detection reaction assay for human identity testing

=> d 52, 53 bib ab

L10 ANSWER 52 OF 58 MEDLINE DUPLICATE 13
AN 1999361785 MEDLINE
DN 99361785 PubMed ID: 10435432
TI The utility of short tandem repeat loci beyond human identification: implications for development of new DNA typing systems.
AU Chakraborty R; Stivers D N; Su B; Zhong Y; Budowle B
CS Human Genetics Center, School of Public Health, University of Texas, Houston, USA.
NC GM 41399 (NIGMS)
GM 52601 (NIGMS)
GM 53545 (NIGMS)
SO ELECTROPHORESIS, (1999 Jun) 20 (8) 1682-96. Ref: 42
Journal code: 8204476. ISSN: 0173-0835.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199909

ED Entered STN: 19991005
Last Updated on STN: 19991005
Entered Medline: 19990922

AB Since the first characterization of the population genetic properties of repeat polymorphisms, the number of short tandem repeat (STR) loci validated for **forensic** use has now grown to at least 13. Worldwide variations of allele frequencies at these loci have been studied, showing that variations of interpopulation diversity at these loci do not compromise the power of identification of individuals. However, data collected for validation of these loci for **forensic** use has utility beyond human identification; the origin and past migration history of modern humans can be reconstructed from worldwide variations at these loci. Furthermore, complex **forensic** cases previously unresolvable can now be investigated with the help of the validated STR loci. Here, we provide the absolute power of the validated set of 13 STR loci for addressing these issues using multilocus genotype data on 1,401 individuals belonging to seven populations (US European-American, US African-American, Jamaican, Italian, Swiss, Chinese and Apache Native-American). Genomic research is discovering new classes of polymorphic loci (such as the **single nucleotide polymorphisms, SNPs**) and lineage markers (such as the mitochondrial DNA and Y-chromosome markers); our aim, therefore, was to determine how many **SNP** loci are needed to match the power of this set of 13 STR loci. We conclude that the current set of STR loci is adequate for addressing most problems of human identification (including interpretations of DNA mixtures). However, if suitable number of **SNPs** are used that would match the power of the STR loci, they alone cannot resolve more complex cases unless they are supplemented by the validated STR loci.

L10 ANSWER 53 OF 58 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 14

AN 1999:368056 BIOSIS

DN PREV199900368056

TI Informativity assessment for biallelic **single nucleotide polymorphisms**.

AU Krawczak, Michael (1)

CS (1) Institute of Medical Genetics, University of Wales College of Medicine, Health Park, Cardiff, CF4 4XN UK

SO Electrophoresis, (June, 1999) Vol. 20, No. 8, pp. 1676-1681.
ISSN: 0173-0835.

DT Article

LA English

SL English

AB Common **single nucleotide polymorphisms** (**SNPs**) have the potential to provide a widely used means of simple and robust kinship testing. Suitable measures of polymorphism informativity are therefore required in order to guide the search for the most efficient combinations of **SNPs**. In the context of kinship testing, such measures should preferably be related to Z, the power of excluding false paternity in trios comprising mother, child and alleged father. Since the bulk of **SNPs** is expected to be biallelic, a Z-related measure of informativity can be defined for **SNPs** in a particularly elegant manner: allele frequency vectors of sets of n biallelic **SNPs** that give rise to the same Z value approximate to an n-dimensional sphere around (1/2,...,1/2). Owing to this relationship, it can be shown that the number N of maximally informative **SNPs** (i.e., of **SNPs** with allele frequencies 1/2), providing the same Z value as a given set of n **SNPs**, approximates to 2n times the average gene diversity of thelatter. Linear regression analysis of a large number of simulated **SNP** sets reveals that only a minor linear correction of N is required for large n. Since Z = 1-(13/16)N, N can also

be calculated easily for multiallelic markers with known Z. The "equivalent number of maximally informative **SNPs**", N, is therefore suggested as a measure of marker informativity in the context of kinship testing.